

Page 1 of 7



RAW SEQUENCE LISTING

DATI

DATE: 03/22/2001 TIME: 16:22:00 **ENTERED**

PATENT APPLICATION: US/09/691,763A

Input Set : A:\E03557003NEW.TXT
Output Set: N:\CRF3\03222001\1691763A.raw

```
4 <110> APPLICANT: Vertino, Paula M.
 6 <120> TITLE OF INVENTION: TMS1 Compositions and Methods of Use
  <130> FILE REFERENCE: E0355/7003/ERG/MAT
11 <140> CURRENT APPLICATION NUMBER: US 09/691,763A
12 <141> CURRENT FILING DATE: 2000-10-18
14 <150> PRIOR APPLICATION NUMBER: US 60/159,975
15 <151> PRIOR FILING DATE: 1999-10-18
17 <160> NUMBER OF SEO ID NOS: 27
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
21 <210> SEO ID NO: 1
22 <211> LENGTH: 2821
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo Sapiens
26 <400> SEQUENCE: 1
    aagettttga atacaacatg etgeaggeat caeageetea tteatteett eacteageaa
    atetttactc agcacctaat gtgttccaga tacattttt tttttcagat ggaatctagc
                                                                           120
    tetgteacce aggetggagt geagtggtge aatettgget eactgtagee tetgeeteeg
                                                                           180
   aggttcaagc gattctcatg cctcagccgc cctagtagct aggattacag gcgccctcca
                                                                           240
31
   ccacacacag ctatttccag gtacattctt gacgctagga attcagcaaa gaataagaca
                                                                           300
   gttaaggtct ccgatgctca taggcctcac attttagaga gggatgaatg tccaataagc
33
   atataaacat ataatatgtc agggtcgtat gactacaagg aacagtgatt gttacaaccc
   agatgagagg gaaaaataaa ggattccaaa tatccccctt gggaagtaga gtcaggattc
34
   aaacaaagaa ctgtatggct tcaagttcat ggtctttaat ctcctggagg ctgtctctct
35
    ttettttte tttttttaa teagtqttqq qateaaatte tqqctcccct aggaageate
36
    tggcaaggtt tcgggagcca tcgggttggc catgttatgc tggaatattt ataagcaccg
37
                                                                           660
                                                                           720
38
    gagggttatc cccatgtcgt agaaaatgaa actgaagctc agagagattt gcactctctg
39
    cccttttgta caactcattt ttccccagta tgtggaattg agggagette acgettetag
                                                                           780
                                                                           840
40
    ctgtcatgat tccaagattc tacgacatgt gggagaggat cctaaggttc ggggaaccgc
                                                                           900
41
    ggaggtttcg gggttctaga aatccgaggt tctaagccta ggtgctccaa taaacccagt
42
    gagagecage ecaggittee ggitetgiace egetggigea ageccagaga caageaggeg
                                                                           960
                                                                          1020
43
    ccacccatga gcccctctgc ggccccctcc cgggtcccac ctcgcaggcc agctggaggg
    cgcgatcctg gcgtcccccg acggcctggg gccccaatcc agaggcctgg gtgggagggg
                                                                          1080
44
45
    accaagggtg tagtaaggaa gcgccttttg ctggagggca acggaccggg gcggggagtc
                                                                          1140
    gggagaccag agtgggagga aggcggggag tccaggttcc gccccggagc cgacttcctc
                                                                          1200
47
    ctggtcggcg gctgcagcgg ggtgagcggc ggcagcggcc ggggatcctg gagccatggg
                                                                          1260
    gegegegege gaegecatee tggatgeget ggagaacetg acegeegagg ageteaagaa
                                                                          1320
                                                                          1380
   gttcaagetg aagetgetgt eggtgeeget gegegaggge taegggegea teeegegggg
                                                                          1440
   egegetgetg tecatggacg cettggacet cacegacaag etggteaget tetacetgga
                                                                          1500
   gacctacggc gccgagctca ccgctaacgt gctgcgcgac atgggcctgc aggagatggc
   egggeagetg eaggeggeea egeaceaggg tgageegeee eegtteeeet ceaceeegte
                                                                          1560
   tttcccctcc acccacacca gegettaccc egegggetet teegetttet gttcctccta
                                                                          1620
   cocctaaaca aagotgotot accggaaagg aggotoccca cgottggoot accgaccaac
                                                                          1680
   gggaccccgg ccccacggcg ggaagggaag ggaaggggat cacttggccc atatccttcc
                                                                          1740
55
                                                                          1800
56
   aggetetgga geogegeag etgggateca ggeeeteet cagteggeag ceaagecagg
   tgaggeetee acacceagee eggeeceace geacteetge acageetgea tetgtgetee
                                                                          1860
57
   cgcaaccagg gcagggcagg gcagggcagg cacggcttgg caaccetgcg caccccaccc
                                                                          1920
                                                                          1980
   accaacccac accetgeggg ggaagggaga caatattacc ctcatcccac tgcatgtggg
```



RAW SEQUENCE LISTING DATE: 03/22/2001 PATENT APPLICATION: US/09/691,763A TIME: 16:22:00

Input Set : A:\E03557003NEW.TXT
Output Set: N:\CRF3\03222001\I691763A.raw

60 gtcctggtgg ccgcccctg gagccctgcc cctaggcttg cagaggaatt cctgaa	agaac 2040
61 tcaaqttcag cagggacagg ccccacaccc tggctgctgg ctcatgttct cctccc	caccc 2100
62 ccaggcctgc actttataga ccagcaccgg gctgcgctta tcgcgagggt cacaaa	acgtt 2160
63 qaqtqqctqc tqqatqctct gtacgggaag gtcctgacgg atgagcagta ccaggo	cagtg 2220
64 cgggccgagc ccaccaaccc aagcaagatg cggaagctct tcagtttcac accago	cctgg 2280
65 aactggacct gcaaggactt gctcctccag gccctaaggg agtcccagtc ctacct	tggtg 2340
66 gaggacetgg ageggagetg aggeteette ceageaacae teeggteage ceetgg	gcaat 2400
67 cccaccaaat catcctgaat ctgatctttt tatacacaat atacgaaaag ccagct	ttgaa 2460
68 cttqtqtqtt ttcctqcttc tagcctqctq gcatqtqcaq agctcaqcta tqcttc	cagag 2520
69 gccacccage etecagetee atgteectag ggtetetgge accceaaatg ettec	
70 ccttcctggt atcgccatgg aatatccctc ctcattcacc aggtggtgct cctcca	agtgc 2640
71 tecetaaagg gtetaacett accattatag ataacageet gtgacecagg teegaa	aggtt 2700
72 aaaagaggca tgtaccaaag ggcgcaaact ggtgggcagc tctgtccaag ccatti	
73 acacactagt cttcataget eccetacett ecacatttte caetggaaga aaaaaa	tggca 2820
74 a	2821
76 <210> SEO ID NO: 2	
77 <211> LENGTH: 770	
78 <212> TYPE: DNA	
79 <213> ORGANISM: Homo Sapiens	
81 <220> FEATURE:	
82 <221> NAME/KEY: CDS	
83 <222> LOCATION: (75)(662)	
85 <400> SEQUENCE: 2	
86 ccacqcqtcc qacttcctcc tggtcggcgg ctgcagcggg gtgagcggcg gcagc	ggccg 60
87 gggateetgg agec atg ggg ege geg ege gae gee ate etg gat geg e	
88 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala 1	Leu
89 1 5 10	
91 gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg	ctg 158
92 Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu	Leu
93 15 20 25	
95 tog gtg cog ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg	ctg 206
96 Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala	Leu
97 30 35 40	
99 ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc	tac 254
100 Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe	Tyr
101 45 50 55	60
103 ctq gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac	atg 302
104 Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp	
105 65 70 75	
107 ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag	ggc 350
108 Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln	Gly
109 80 85 90	
111 tet gga gee geg eea get ggg ate eag gee eet eet eag teg gea	gcc 398
112 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala	
113 95 100 105	
115 aag cca ggc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc	gcg 446
116 Lys Pro Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile	Ala
117 110 115 120	
119 agg gtc aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag	gtc 494
TTO MED 200 TOW WAS 200 200 200 200 200 200 200 200 200	-

RAW SEQUENCE LISTING DATE: 03/22/2001 PATENT APPLICATION: US/09/691,763A TIME: 16:22:00

Input Set : A:\E03557003NEW.TXT Output Set: N:\CRF3\03222001\I691763A.raw

120	Output Set: N:\CRF3\03222001\I691763A.raw	
Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro 125 127 39c aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc 128 Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr 129 160 1155 1170 121 122 123 125 126 127 128 129 129 129 120 120 121 120 121 121		
125	123 ctg acg gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca	542
127 agc aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc 590 128 Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr 160	124 Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro	
Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr	125 145 150 155	
129	127 age aag atg egg aag ete tte agt tte aca eea gee tgg aac tgg ace	590
131 tgc aag gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg 638 132 Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu 185 135 gtg gag gac ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc 692 136 Val Glu Asp Leu Glu Arg Ser * 190 195 139 cctggcaatc ccaccaaatc atcctgaatc tgatctttt atacacaata tacgaaaagc 752 140 cagcttgaaa aaaaaaaa 770 142 C210> SEO ID NO: 3 3 3 (211> LENGTH: 195 144 (212> TYPE: PRT 145 (212> TYPE: PRT 145 (212> TYPE: PRT 146 (212> TYPE: PRT 147 (400> SEOUENCE: 3 148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr 149	128 Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr	
132 Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu 133 175 180 185 185 185 185 185 185 175 180 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185 185	129 160 165 170	
133	131 tgc aag gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg	638
135 9tg gag gac ctg gag ctg agc ttg ggetcettec cagcaacact ccggtcagcc 136 Val Glu Asp Leu Glu Arg Ser * 190 195 193 195 193 195 193 195 193 195 193 195 193 195 193 195 193 195 193 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 195 1	132 Cys Lys Asp Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu	
136	133 175 180 . 185	
137	135 gtg gag gac etg gag egg age tga ggeteettee cageaacaet eeggteagee	692
139	136 Val Glu Asp Leu Glu Arg Ser *	
140	137 190 195	
142 <210> SEQ ID NO: 3 143 <211> LENGTH: 195 144 <212> TYPE: PRT 145 <213> ORGANISM: HOMO Sapiens 147 <400> SEQUENCE: 3 148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr 149	139 cctggcaatc ccaccaaatc atcctgaatc tgatctttt atacacaata tacgaaaagc	752
143 <211> LENGTH: 195 144 <212> TYPE: PRT 145 <213> ORGANISM: Homo Sapiens 147 <400> SEQUENCE: 3 148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr 149 1 5 10 15 150 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu 151 20 25 30 152 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp 153 35 40 45 154 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr 155 50 50 60 156 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu 157 65 70 70 75 80 158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala 159 85 90 95 160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 161 100 105 162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn 163 115 120 164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 125 150 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 150 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 195 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4	140 cagcttgaaa aaaaaaaa	770
144 <212> TYPE: PRT 145 <213> ORGANISM: Homo Sapiens 147 <400> SEQUENCE: 3 148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr 149 1 5 150 150 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu 151 20 30 152 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Glu Thr Tyr 153 35 40 45 154 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr 155 50 50 55 60 156 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu 157 65 70 70 70 80 158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala 159 85 90 95 160 Pro Ala Gly Ile Gln Ala Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 161 100 105 162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn 163 115 120 125 164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 135 150 160 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 150 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 195 175 <210> SEQ ID NO: 4	142 <210> SEQ ID NO: 3	
145 < 213 > ORGANISM: Homo Sapiens 147 < 4000 > SEQUENCE: 3 148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr 149	143 <211> LENGTH: 195	
147 <400> SEQUENCE: 3 148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr 149 1 5 15 150 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu 151 20 25 30 152 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp 153 35 40 45 154 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr 155 50 55 60 156 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu 157 65 70 70 75 80 158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala 159 95 160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 161 100 105 162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn 163 115 164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 135 150 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 160 Ala Ser 170 180 See Ilb NO: 4	144 <212> TYPE: PRT	
148	145 <213> ORGANISM: Homo Sapiens	
149	147 <400> SEQUENCE: 3	
150 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu 151	148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr	
151	149 1 5 10 15	
152 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp 153	150 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu	
153	151 20 25 30	
154 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr 155 50 50 55 70 60 156 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu 157 65 70 70 75 80 158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala 159 85 90 95 160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 161 100 105 110 162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn 163 115 120 125 164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 135 135 140 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 150 155 155 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 160 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 195 175 <210> SEQ ID NO: 4	152 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp	
155	153 35 40 45	
156 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu 157 65 70 75 80 158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala 159 90 95 160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 161 100 105 110 162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn 163 115 120 125 164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 135 140 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 155 160 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 165 170 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 195 175 <210> SEQ ID NO: 4	154 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr	
157 65 70 70 75 80 158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala Ala 159 90 95 160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 100 100 110 110 110 110 110 110 110 11	155 50 55 60	
158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala 159 85 90 95 160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 161 100 105 162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn 163 115 120 125 164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 135 140 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 150 155 160 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 160 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4		
159		
160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu 161	•	
161		
162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn 163 115 120 125 164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 135 140 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 167 145 150 155 160 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 175 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 190 172 Glu Arg Ser 195 195 175 2210> SEQ ID NO: 4		
163		
164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu 165 130 135 140 166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 150 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 165 170 170 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4	• -	
165		
166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg 167 145 150 150 155 160 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 165 170 170 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4		
167 145 150 155 160 168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 165 170 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4		
168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu 169 165 170 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4		
169 165 170 175 170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4	167 145 150 155 160	
170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu 171 180 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4		
171 180 185 190 172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4		
172 Glu Arg Ser 173 195 175 <210> SEQ ID NO: 4		
173 195 175 <210> SEQ ID NO: 4		
175 <210> SEQ ID NO: 4		
·		
1/6 <211> LENGTH: 626	176 <211> LENGTH: 626	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/691,763A DATE: 03/22/2001 TIME: 16:22:00

Input Set : A:\E03557003NEW.TXT
Output Set: N:\CRF3\03222001\1691763A.raw

177	<212> TYPE: DNA				
178	<213> ORGANISM: Homo S	apiens			
180	<400> SEQUENCE: 4	•			
181	agcgcctttt gctggagggc	aacggaccg	g ggcggggagt	cgggagacca gagtgg	gagg 60
182	aaggcgggga gtccaggttc	cgccccgga	g ccgacttcct	cctggtcggc ggctgca	agcg 120
183	gggtgagcgg cggcagcggc	cggggatcci	t ggagccatgg	ggcgcgcgcg cgacgc	catc 180
184	ctggatgcgc tggagaacct	gaccgccgag	g gagctcaaga	agttcaagct gaagct	gctg 240
185	teggtgeege tgegegaggg	ctacgggcg	c atcccgcggg	gegegetget gtecate	gac 300
186	geettggace teacegacaa	gctggtcag	c ttctacctgg	agacctacgg cgccgag	gctc 360
187	accgctaacg tgctgcgcga	catgggcctg	g caggagatgg	ccgggcaget gcagge	gcc 420
188	acgcaccagg gtgagccgcc	cccgttcccc	c tccaccccgt	ctttcccctc caccca	cacc 480
189	agcgettace eegegggete	ttccgctttc	c tgttcctcct	accectaaac aaagete	icte 540
190	taccggaaag gaggctcccc	acgcttggc	c taccgaccaa	cgggaccccg gccccad	egge 600
191			-		626
193	<210> SEQ ID NO: 5				
194	<211> LENGTH: 340				
195	<212> TYPE: DNA				
196	<213> ORGANISM: Homo Sa	apiens			
	<220> FEATURE:	-			
199	<221> NAME/KEY: CDS				
200	<222> LOCATION: (67)	. (339)			
	<400> SEQUENCE: 5	` '			
203	cegaettect cetggtegge	ggctgcagc	a qaqtqaqcqq	cadcadedde edddaat	cct 60
204	ggagee atg ggg ege geg				
205				Asp Ala Leu Glu Asr	
206					
200	1	5		10	•
208	-	=		10	
	ctg acc gcc gag gag ct	tc aag aag	ttc aag ctg	10 aag ctg ctg tcg gt	.g 156
208	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le	tc aag aag	ttc aag ctg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va	.g 156
208 209	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20	ttc aag ctg Phe Lys Leu 25	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va	ig 156 il
208 209 210	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 ccg ctg cgc gag ggc ta	tc aag aag eu Lys Lys 20 ac ggg cgc	ttc aag ctg Phe Lys Leu 25 atc ccg cgg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc	2g 156 11 80 ec 204
208 209 210 212	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc	ttc aag ctg Phe Lys Leu 25 atc ccg cgg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc	2g 156 11 80 ec 204
208 209 210 212 213	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 2 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly Ty 35	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se	156 11 30 30 30 31 32 32 34
208 209 210 212 213 214	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly Ty 35 atg gac gcc ttg gac ct	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se 45 agc ttc tac ctg ga	29 156 11 20 204 20 204 21 252
208 209 210 212 213 214 216	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 2 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly Ty 35	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se 45 agc ttc tac ctg ga	29 156 11 20 204 20 204 21 252
208 209 210 212 213 214 216 217	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly Ty 35 atg gac gcc ttg gac ct Met Asp Ala Leu Asp Le	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl	156 11 10 10 10 10 20 204 27 29 252
208 209 210 212 213 214 216 217 218	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se agc ttc tac ctg ga Ser Phe Tyr Leu Gl 60 cgc gac atg ggc ct	156 11 10 10 20 204 27 29 252 20 20 300
208 209 210 212 213 214 216 217 218 220	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly Ty 35 atg gac gcc ttg gac ct Met Asp Ala Leu Asp Le	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se agc ttc tac ctg ga Ser Phe Tyr Leu Gl 60 cgc gac atg ggc ct	156 11 10 10 20 204 27 29 252 20 20 300
208 209 210 212 213 214 216 217 218 220 221	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly 35 atg gac gcc ttg gac ct Met Asp Ala Leu Asp Le 50 acc tac ggc gcc gag ct Thr Tyr Gly Ala Glu Le	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu	aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se agc ttc tac ctg ga Ser Phe Tyr Leu Gl cgc gac atg ggc ct Arg Asp Met Gly Le	156 11 10 10 20 204 27 29 252 20 20 300
208 209 210 212 213 214 216 217 218 220 221 222	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly Ty 35 atg gac gcc ttg gac ct Met Asp Ala Leu Asp Le 50 acc tac ggc gcc gag ct Thr Tyr Gly Ala Glu Le 65 cag gag atg gcc ggg ca	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70 ag ctg cag	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl Cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g	156 11 100 204 204 21 252 u 252 u 300 uu
208 209 210 212 213 214 216 217 218 220 221 222 224	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15 ccg ctg cgc gag ggc ta Pro Leu Arg Glu Gly 35 atg gac gcc ttg gac ct Met Asp Ala Leu Asp Le 50 acc tac ggc gcc gag ct Thr Tyr Gly Ala Glu Le	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Th Ala ag ctg cag ln Leu Gln	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tcg Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln	156 11 100 204 204 21 252 u 252 u 300 uu
208 209 210 212 213 214 216 217 218 220 221 222 224 225 226	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70 ag ctg cag	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl Cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g	156 11 100 204 204 21 252 u 252 u 300 uu
208 209 210 212 213 214 216 217 218 220 221 222 224 225 226 229	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Th Ala ag ctg cag ln Leu Gln	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tcg Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln	156 11 100 204 204 21 252 u 252 u 300 uu
208 209 210 212 213 214 216 217 218 220 221 222 224 225 226 229 230	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Th Ala ag ctg cag ln Leu Gln	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tcg Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln	156 11 100 204 204 21 252 u 252 u 300 uu
208 209 210 212 213 214 216 217 218 220 221 222 224 225 226 229 230 231	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70 ag ctg cag ln Leu Gln 85	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tcg Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln	156 11 100 204 204 21 252 u 252 u 300 uu
208 209 210 212 213 214 216 217 218 220 221 222 224 225 226 229 230 231 232	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70 ag ctg cag ln Leu Gln 85	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tcg Gly Ala Leu Leu Se 45 agc ttc tac ctg ga Ser Phe Tyr Leu Gl cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln	156 11 100 204 204 21 252 u 252 u 300 uu
208 209 210 212 213 214 216 217 218 220 221 222 224 225 226 229 230 231 232	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70 ag ctg cag ln Leu Gln 85	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg Ala Ala Thr	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se agc ttc tac ctg ga Ser Phe Tyr Leu Gl 60 cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln 90	156 11 10 10 10 10 10 10 10 10 10 10 10 10
2088 2099 2100 2122 213 2144 2167 2218 2220 2244 2255 2266 2299 2300 2311 2322 2344 235	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70 ag ctg cag ln Leu Gln 85	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg Ala Ala Thr	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se agc ttc tac ctg ga Ser Phe Tyr Leu Gl 60 cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln 90 Leu Glu Asn Leu Th	156 11 10 10 10 10 10 10 10 10 10 10 10 10
208 209 210 212 213 214 216 217 218 220 221 222 224 225 226 229 230 231 232 234	ctg acc gcc gag gag ct Leu Thr Ala Glu Glu Le 15	tc aag aag eu Lys Lys 20 ac ggg cgc yr Gly Arg tc acc gac eu Thr Asp tc acc gct eu Thr Ala 70 ag ctg cag ln Leu Gln 85	ttc aag ctg Phe Lys Leu 25 atc ccg cgg Ile Pro Arg 40 aag ctg gtc Lys Leu Val 55 aac gtg ctg Asn Val Leu gcg gcc acg Ala Ala Thr	10 aag ctg ctg tcg gt Lys Leu Leu Ser Va ggc gcg ctg ctg tc Gly Ala Leu Leu Se A5 agc ttc tac ctg ga Ser Phe Tyr Leu Gl Cgc gac atg ggc ct Arg Asp Met Gly Le 75 cac cag g His Gln 90 Leu Glu Asn Leu Th 15	156 11 10 10 10 10 10 10 10 10 10 10 10 10

PATENT APPLICATION: US/09/691,763A TIME: 16:22:00 Input Set : A:\E03557003NEW.TXT Output Set: N:\CRF3\03222001\1691763A.raw 25 239 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp 35 40 240 241 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr 242 50 55 60 243 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu 244 65 70 75 80 70 245 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln 246 85 248 <210> SEQ ID NO: 7 249 <211> LENGTH: 57 250 <212> TYPE: DNA 251 <213> ORGANISM: Homo Sapiens 253 <220> FEATURE: 254 <221> NAME/KEY: CDS 255 <222> LOCATION: (3)...(56) 257 <400> SEQUENCE: 7 258 gc tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala 260 262 gcc aag cca g 263 Ala Lys Pro 267 <210> SEQ ID NO: 8 268 <211> LENGTH: 18 269 <212> TYPE: PRT 270 <213> ORGANISM: Homo Sapiens 272 <400> SEQUENCE: 8 273 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala 274 1 5 10 275 Lys Pro 278 <210> SEQ ID NO: 9 279 <211> LENGTH: 356 280 <212> TYPE: DNA 281 <213> ORGANISM: Homo Sapiens 283 <220> FEATURE: 284 <221> NAME/KEY: CDS 285 <222> LOCATION: (3)...(258) 287 <400> SEQUENCE: 9 288 gc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc 289 Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val 290 5 10 292 aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg 293 Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr 294 20 25 30 95 gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag 297 Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys 298 35 40 45 143 300 atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag 191 301 Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys

DATE: 03/22/2001

RAW SEQUENCE LISTING

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/691,763A

DATE: 03/22/2001 TIME: 16:22:01

Input Set : A:\E03557003NEW.TXT

Output Set: N:\CRF3\03222001\1691763A.raw

L:309 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:530 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:530 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:581 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:581 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:581 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23